

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/360,242

Art Unit / Team No. :

01PE

Date Processed by STIC:

8/10/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

8360

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION**SERIAL NUMBER:**09/360,242**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 **Misaligned Amino Acid
Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

- 8 **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 10 **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 **Use of <213>Organism
(NEW RULES)** Sequence(s) are missing this mandatory field or its response.

- 12 **Use of <220>Feature
(NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/360,242

DATE: 08/10/1999

TIME: 10:37:55

Input Set: I360242.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

even throughout

1 <110> McDonald, John R.
2 Coggins, Philip
3 <120> METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
4 OTHER INFLAMMATORY CONDITIONS AND DISORDERS
5 <130> 25020-601B
6 <140> US/09/360,242
7 <141> 1999-07-22
8 <160> 70
9 <170> FastSEQ for Windows Version 3.0

ERRORED SEQUENCES FOLLOW

10 <210> 40
11 <211> 88
12 <212> DNA
13 <213> Artificial Sequence
14 <220>
15 <223> Homo sapien His-Tag leader sequence
16 <400> 40
E--> 17 aaggagatatacc atg ggc agc agc cat cat cat cat cat cac agc agc
18 Met Gly Ser Ser His His His His His His Ser Ser
19 1 5 10
20 ggc ctg gtg ccg cgc ggc agc cat atg ctc gag gat ccg
21 Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro
22 15 20 25

(43) 49

(82) 88

23 <210> 54
24 <211> 999
25 <212> DNA
26 <213> Artificial Sequence
27 <220>
28 <221> CDS
29 <222> (1)..(999)
30 <220>
31 <223> Description of Artificial Sequence: Construct encoding chemokine-
32 toxin fussion protein MCP1-AM-SAPORIN
33 <400> 54
34 atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
35 Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
36 1 5 10 15
37 acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
38 Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/360,242

DATE: 08/10/1999

TIME: 10:37:55

Input Set: I360242.RAW

39		20		25		30		
40	acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg							144
41	Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val							
42		35		40		45		
43	gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc							192
44	Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser							
45		50		55		60		
46	atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg gtt							240
47	Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Val							
48		65		70		75		80
49	act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc							288
50	Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser							
51			85		90		95	
52	agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa							336
53	Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys							
54		100		105		110		
55	tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag							384
56	Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys							
57		115		120		125		
58	ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc							432
59	Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly							
60		130		135		140		
61	ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat							480
62	Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn							
63		145		150		155		160
64	acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg							528
65	Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala							
66		165		170		175		
67	gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca							576
68	Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala							
69		180		185		190		
70	ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc							624
71	Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile							
72		195		200		205		
73	acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg							672
74	Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu							
75		210		215		220		
76	ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa							720
77	Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys							
78		225		230		235		240
79	gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc							768
80	Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala							
81		245		250		255		
82	gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac							816
83	Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn							
84		260		265		270		
85	aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa							864
86	Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys							
87		275		280		285		
88	aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat							912

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/360,242

DATE: 08/10/1999

TIME: 10:37:55

Input Set: I360242.RAW

89	Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn	
90	290 295 300	
91	aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg	960
92	Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu	
93	305 310 315 320	
94	caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa	999
95	Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
96	325 330	
E--> 97	325 330	

delete (dephmented)

see following pages for more errors

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/360,242

DATE: 08/11/1999
TIME: 09:21:20

Input Set: I360242.RAW

95 <210> SEQ ID NO 10
96 <211> LENGTH: 5
97 <212> TYPE: PRT
98 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Artificial Sequence
101 <400> SEQUENCE: 10
102 Ser Gly Ser Ser Cys
103 1 5
104 <210> SEQ ID NO 11
105 <211> LENGTH: 28
106 <212> TYPE: PRT
107 <213> ORGANISM: diphtheria toxin trypsin sensitive linker
108 <400> SEQUENCE: 11
109 Ala Met Gly Arg Ser Gly Gly Gly Cys Ala Gly Asn Arg Val Gly Ser
110 1 5 10 15
111 Ser Leu Ser Cys Gly Gly Leu Asn Leu Gln Ala Met
112 20 25
113 <210> SEQ ID NO 12
114 <211> LENGTH: 6
115 <212> TYPE: PRT
116 <213> ORGANISM: homo sapien
117 <220> FEATURE:
118 <221> NAME/KEY: REPEAT
119 <222> LOCATION: (3)...(3)
120 <223> OTHER INFORMATION: repeat unit 2-4 times
121 <220> FEATURE:
122 <221> NAME/KEY: REPEAT
123 <222> LOCATION: (3)...(4)
124 <223> OTHER INFORMATION: repeat family 1-11 times
125 <400> SEQUENCE: 12
126 Ala Met Gly Ser Ala Met
127 1 5
128 <210> SEQ ID NO 13
129 <211> LENGTH: 74
130 <212> TYPE: PRT
131 <213> ORGANISM: homo sapien
132 <400> SEQUENCE: 13
133 Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn Arg
134 1 5 10 15
135 Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser Gly
136 20 25 30
137 Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys Asp
138 35 40 45
139 Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys Tyr
140 50 55 60
141 Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
142 65 70
143 <210> SEQ ID NO 14
144 <211> LENGTH: 77

*This does not replace source of
genetic material.*

*See circled portion
of item 12 on Enon
summary sheet*

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/360,242

DATE: 08/11/1999
TIME: 09:21:20

Input Set: I360242.RAW

```

195 <211> LENGTH: 73
196 <212> TYPE: PRT
197 <213> ORGANISM: homo sapien
198 <400> SEQUENCE: 17
199   Lys Ser Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu
200     1             5             10             15
201   Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser
202             20             25             30
203   Ile Cys Ser Asn Glu Gly Leu Ile Phe Lys Leu Lys Arg Gly Lys Glu
204             35             40             45
205   Ala Cys Ala Leu Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met
206             50             55             60
207   Leu Arg His Cys Pro Ser Lys Arg Lys
208     65             70
209 <210> SEQ ID NO 18
210 <211> LENGTH: 133
211 <212> TYPE: PRT
212 <213> ORGANISM: homo sapien
213 <400> SEQUENCE: 18
214   Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp Val Asn Cys
215     1             5             10             15
216   Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
217             20             25             30
218   Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
219             35             40             45
220   Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
221             50             55             60
222   Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
223     65             70             75             80
224   Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
225             85             90             95
226   Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
227             100            105            110
228   Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
229             115            120            125
230   Ser Leu Ala Ile Phe
231     130
232 <210> SEQ ID NO 19
233 <211> LENGTH: 77
234 <212> TYPE: PRT
235 <213> ORGANISM: homo sapien
236 <400> SEQUENCE: 19
237   Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys
238     1             5             10             15
239   Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val
240             20             25             30
241   Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys Leu
242             35             40             45
243   Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln
244     50             55             60

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

✓ FYI